

DB	61	IPKEGGLSFMRGNLANIYIRFFPQALNFAFKDKTKOFLGCVGDHKKQFWKRFAGNLSG	120
QY	121	GAAGATSLCFYVPLDFARTRLAADYKSGSTEREFRLGCDLCLKITKSDGIRGLYOGFSVS	180
DB	121	GAAGATSLCFYVPLDFARTRLAADYKSGAARREFSGLNCNLITKIRKSDGIRGLYOGFSVS	180
QY	181	VGGIITVAAAFGVYDTAKGMLPDRKNHIYVSMIAQTVAACVSVYPRFTVRRMM	240
DB	181	VGGIITVAAAFGVYDTAKGMLPDRKNHIYVSMIAQTVAACVSVYPRFTVRRMM	240
QY	241	OSGRKGADIMYTGTVDCMKRIFRDEGKAFFGAGMSNVLRGGAFAVLVYDELKKVI	298
DB	241	OSGRKGADIMYTGTVDCMKRIAKDEGAKAFAFGAGMSNVLRGGAFAVLVYDELKKYV	298
RESULT	2		
QY19M9	0919M9	PRELIMINARY; PRT; 298 AA.	
AC	0919M9		
DT	01-OCT-2000 (Tremblrel. 15, Created)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-OCT-2000 (Tremblrel. 15, Last annotation update)		
DE	ADENINE NUCLEOTIDE TRANSLOCASE.		
GN	ANT1.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Crawford M.J., Khosrowshahan F., Varmuza S.L., Liversage R.A.;		
RT	"Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and		
RT	Dynamic Patterns of Expression During Development."		
RL	Submitted (FE8-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF231347; AAF63471.1; --		
SO	SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;		
	Query Match	92.1%; Score 1421; DB 13; Length 298;	
	Best Local Similarity	90.3%; Pred. No. 3,8e-122;	
	Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;		
QY	1	MTEQAISFAKDFLAGGIAAISKTAVAPIERVKLLLOYOHASKQIADKQYGIYDCIVR	60
DB	1	MTDAISFAKDFLAGGVAASIKTVADPIERVKLLLOYOHASKQIADKKNYKGIYDCIVR	60
QY	61	IPKEGVSPFMGNLANIYIRFFPQALNFAFKDKTKOFLGCVGDHKKQFWKRFAGNLSG	120
DB	61	IPKEGVSPFMGNLANIYIRFFPQALNFAFKDKTKKFLDNDVDDTKQFWKRFAGNLSG	120
QY	121	GAAGATSLCFYVPLDFARTRLAADYKSGSTEREFRLGCDLCLKITKSDGIRGLYOGFSVS	180
DB	121	GAAGATSLCFYVPLDFARTRLAADYKSGAAREFRLGCDLCLKITKSDGIRGLYOGFSVS	180
QY	181	VGGIITVAAAFGVYDTAKGMLPDRKNHIYVSMIAQTVAACVSVYPRFTVRRMM	240
DB	181	VGGIITVAAAFGVYDTAKGMLPDRKNHIYVSMIAQTVAACVSVYPRFTVRRMM	240
QY	241	OSGRKGADIMYTGTVDCMKRIFRDEGKAFFGAGMSNVLRGGAFAVLVYDELKKVI	298
DB	241	OSGRKGADIMYSGTIDCKKRIARDGSKAFAFGAGMSNVLRGGAFAVLVYDELKKVI	298
RESULT	3		
ID	062164	PRELIMINARY; PRT; 298 AA.	
AC	062164		
DT	01-NOV-1996 (Tremblrel. 01, Created)		
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)		
DT	01-OCT-2000 (Tremblrel. 15, Last annotation update)		
DE	ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1).		
GN	MANCI OR ANT1.		

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=MUSCLE;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; X74510; CAA52616.1; -.
DR EMBL; AF240002; AAF64470.1; -.
DR INTERPRO: IPR001993; -.
DR INTERPRO: IPR002067; -.
DR INTERPRO: IPR002113; -.
DR PFAM; PF00153; mito_carr; 1.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00927; ADPTRNSLASE.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0991462 CRC64;

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Query Match	Similarity	88.9%	Pred. No. 7.2e-122	Matches 265	Conservative 19	Mismatches 14	Indels 0	Gaps 0
QY	1 MTEQAI\$FAKDFLAGGIAAISKTA\$VAPIERVKLLQVOHASKQIADADKQYKGI\$VDCIVR 60							
Db	1 .MDDQAL\$FLKDFLAGGIAA\$VSKTA\$VAPIERVKLLQVOHASKQI\$ADKQYKGI\$D\$CIVR 60							
QY	61 IPKEGVLS\$FPMGNLANIYRPTQALNPA\$FDKTKQYKQFLG\$VDNHPQ\$FWR\$FAGNLASG 120							
Db	61 IPKEGVLS\$FPMGNLANIYRPTQALNPA\$FDKTKQYKQFLG\$VDNHPQ\$FWR\$FAGNLASG 120							
QY	121 GAAGAT\$SLCEVYPLD\$FARTRLAADV\$GSGTERE\$RFGLD\$LVK\$ITKSDG\$INGLYOG\$F\$VS 180							
Db	121 GAAGAT\$SLCEVYPLD\$FARTRLAADV\$GSGTERE\$RFGLD\$LVK\$ITKSDG\$INGLYOG\$F\$VS 180							
QY	181 VQGIIT\$YRAATY\$GVYD\$TAKGMLP\$D\$KNNHIY\$VSM\$IAQTV\$R\$VAGV\$SY\$P\$D\$TV\$RR\$MM 240							
Db	181 VQGIIT\$YRAATY\$GVYD\$TAKGMLP\$D\$KNNHIY\$VSM\$IAQTV\$R\$VAGV\$SY\$P\$D\$TV\$RR\$MM 240							
QY	241 QSGRGADIMYTG\$YD\$CNRKIF\$RDEG\$GK\$AF\$FGAMS\$NVL\$RG\$G\$AF\$V\$L\$V\$DEL\$K\$VI 298							
Db	241 QSGRGADIMYTG\$YD\$CNRKIA\$DKG\$AN\$AF\$FGAMS\$NVL\$RG\$G\$AF\$V\$L\$V\$DEL\$K\$VI 298							
RESULT 4								
Q9PRH1	PRELIMINARY:	PRT:	298 AA.					
AC	Q9PRH1:							
DT	01-MAY-2000 (TREM\$BL\$REL. 13, Created)							
DT	01-MAY-2000 (TREM\$BL\$REL. 13, Last sequence update)							
DT	01-JUN-2000 (TREM\$BL\$REL. 14, Last annotation update)							
DE	ADP/ATP TRANSLOCASE.							
OS	Rana rugosa (Frog) .							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.							
OX	NCBI_TaxID=8410;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RA	Mura I., Ohnari H., Nakamura M., Ichikawa Y., Saitoh K.;							
RT	"The origin and differentiation of the heteromorphic sex chromosomes of							
RT	Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of							


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RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
DR EMBL: AB008463; BAA36513.1; -
DR EMBL: AB008456; BAA36506.1; -
DR EMBL: AB008461; BAA36511.1; -
DR EMBL: AB008462; BAA36512.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002030; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito.carr. 1.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
Best Local Similarity 88.6%; Pred. No. 4,8e-121;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQKGYVDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLQVQHSKQITADKQKGYIMDCVVR 60

QY 61 IPKEQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGGVDKHTQFMRYFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGNVDKRTQFMRYFAGNLASG 120

QY 121 GAAGATSLCFYVPLDFAFTRTLAADVGKSGTEREFGGLDCLVTKTSGIRGLYOGFSVS 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYVPLDFAFTRTLAADVGKAGADREFGLDCLAKIFKSPGLKGLYOGFSVS 180

QY 181 VGGIITVAAAFGVYDPAKGLPDPKKNHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIITVAAAFGVYDPAKGLPDPKKNHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240

QY 241 QSGRKGADIMYTGVDCKRIKIFRDEGKAFKFGKAMSNVLRMGCAFVLVLYDELKVI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGAEIMYSGTIDCKKRIARDEGSRAPFKGAMSNVLRMGCAFVLVLYDELKVI 298

RESULT 5
09PRH2 PRELIMINARY: PRT: 298 AA.
AC 09PRH2:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorph sex chromosomes
   Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
   a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
DR EMBL: AB008460; BAA36510.1; -
DR EMBL: AB008458; BAA36508.1; -
DR EMBL: AB008459; BAA36509.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002030; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito.carr. 1.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PS00215; MITOCH_CARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.

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DR PROSITE: PS00215; MITOCH_CARRIER. 3.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 9e-121;
Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQKGYVDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLQVQHSKQITADKQKGYIMDCVVR 60

QY 61 IPKEQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGGVDKHTQFMRYFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGNVDKRTQFMRYFAGNLASG 120

QY 121 GAAGATSLCFYVPLDFAFTRTLAADVGKSGTEREFGGLDCLVTKTSGIRGLYOGFSVS 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYVPLDFAFTRTLAADVGKAGADREFGLDCLAKIFRSDGLKGLYOGFSVS 180

QY 181 VGGIITVAAAFGVYDPAKGLPDPKKNHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VGGIITVAAAFGVYDPAKGLPDPKKNHIYVSMIAQTVTAAGVVSYPEDTVRRMM 240

QY 241 QSGRKGADIMYTGVDCKRIKIFRDEGKAFKFGKAMSNVLRMGCAFVLVLYDELKVI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGAEIMYSGTIDCKKRIARDEGSRAPFKGAMSNVLRMGCAFVLVLYDELKVI 298

RESULT 6
09YIC4 PRELIMINARY: PRT: 298 AA.
AC 09YIC4:
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorph sex chromosomes
   Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
   a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
   INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002030; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito.carr. 1.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PS00215; MITOCH_CARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
Best Local Similarity 87.9%; Pred. No. 2.1e-120;
Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQKGYVDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLQVQHSKQITADKQKGYIMDCVVR 60

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Oy 61 IPKEGVLSFWKGNLANVIRFPTQALNFAEKDKYKQJFLGVDKHTQFMRYFAENLASG 120
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 61 IPKEGVLSFWKGNLANVIRFPTQALNFAEKDKYKQJFLGVDKHTQFMRYFAENLASG 120
Oy 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKRSGIRGLYOGFSVS 180
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKRSGIRGLYOGFSVS 180
Oy 181 VGGIITFAAEVGYVDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSGSPEDTVRRMM 240
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 181 VGGIITFAAEVGYVDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSGSPEDTVRRMM 240
Oy 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFKFGKANSVNLKRGKAFVLYLDELKVI 238
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFKFGKANSVNLKRGKAFVLYLDELKVI 238

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RESULT 7
Oy1336 PRELIMINARY; PRT; 317 AA.
AC O91336;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana sylvatica (wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=45438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=97398141; PubMed=9256066;
R Cai O., Greenway S.C., Storey K.B.;
RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
in wood frogs under freezing stress.";
RL Biochim. Biophys. Acta 1353:69-78(1997).
RN [2]
RP REVISIONS.
R Cai O., Storey K.B.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1 INNER MEMBRANE (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: U04832; AAA97882.2;
DR INTERPRO: IPR001993;
DR INTERPRO: IPR002067;
DR INTERPRO: IPR002113;
DR PRAM: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

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Query Match 81.6%; Score 1259; DB 13; Length 317;
Best Local Similarity 86.8%; Pred. No. 2.8e-107;
Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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Oy 1 MTEQAISFAKDFLAGGIAAISKTAAPVIERVKLLLOVHNSKOIADKOYKGIIVDCIVR 60
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MTDAAISFAKDFLAGGIAAISKTAAPVIERVKLLLOVHNSKOIADKOYKGIIVDCIVR 60
Oy 61 IPKQGVLSFWKGNLANVIRFPTQALNFAEKDKYKQJFLGVDKHTQFMRYFAENLASG 120
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 61 IPKQGVLSFWKGNLANVIRFPTQALNFAEKDKYKQJFLGVDKHTQFMRYFAENLASG 120
Oy 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKRSGIRGLYOGFSVS 180
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKRSGIRGLYOGFSVS 180

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Oy 181 VGGIITFAAEVGYVDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSGSPEDTVRRMM 240
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 181 VGGIITFAAEVGYVDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSGSPEDTVRRMM 240
Oy 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFK 272
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFK 272

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RESULT 8
Oy9VZ70 PRELIMINARY; PRT; 299 AA.
AC O9VZ70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE SESB PROTEIN.
GN SESB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyraoidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731137;
R Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
R Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
R Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
R Abril J.F., Agbayani A., An H.-J., Andrews Pfennoch C., Baldwin D.,
R Balcer R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R Borkova D., Botchan M.R., Bouck J., Broksstein P., Brotlier P.,
R Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
R de Pablo S., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
R Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
R Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
R Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
R Harlin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
R Jatala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
R Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
R Merkulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,
R Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
R Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
R Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
R Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
R Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R Stryckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
R Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
R Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
R Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
R Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2193(2000).
DR EMBL: AE003484; AAF47957.1;
DR FLYBASE: FBgn0003360; seSB.
DR INTERPRO: IPR001993;
DR INTERPRO: IPR002067;
DR INTERPRO: IPR002113;
DR PRAM: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.

```

DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SO SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;

Query Match	81.3%	Score 1254.5	Length 299
Best Local Similarity	80.6%	Pred. NO. 6.7e-107	
Matches 237	Conservative 23	Mismatches 33	Indels 1
			Gaps 1

[illegible]

RESULT	9	
09NHM5		
ID	09NHM5	PRELIMINARY; PRT; 300 AA.
AC	09NHM5	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, last annotation update)	
DE	ADP/ATP TRANSLOCASE.	
OS	Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Oestroidea; Calliphoridae; Lucilia.	
OX	NCBI_TaxID=7375;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SS MAL SEEKING;	
RA	Chen Z., Fair J.A., Batterham P.;	
RT	"A cDNA clone encoding the ADP/ATP translocase of <i>Lucilia cuprina</i> ."	
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF18587; AF32322.1;	
DQ	SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;	

Query Match	80.1%	Score 1235.5	DB 5	Length 300
Best Local Similarity	79.5%	Pred. No. 3.7e-105		
Matches 233	Conservative 24	Mismatches 35	Indels 1	Gaps 1

[illegible]

Db 248 ATEIYKNLHCWATIAQEGTGAFKGAFSNVLRTGGAFLVLYDEIKKL 3000

RESULT	10
044093	
ID	044093
AC	044093;
DT	01-JUN-1998 (TREMBLrel. 06, Created)
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	ADP/ATP TRANSLOCASE (FRAGMENT).
GN	SESB.
OS	Drosophila pseudoobscura (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephyridioidea; Drosophilidae; Drosophila.
OX	NCBI_TaxId=7237;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Zeng L.-W., Cameron J.M., Chen B., Kreitman M.;
RL	Genetica 0:0-0(1997).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC	-1- INNER MEMBRANE (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC	EMBL: AF025798; AAB87883.1; -
DR	FWLBASE: FBgn0023292; Dpse\sesb.
DR	INTERPRO: IPR001993; -
DR	INTERPRO: IPR002067; -
DR	INTERPRO: IPR002113; -
DR	PFAM: PF00153; mito_carr; 1.
DR	PRINTS: PR00926; MITOCARRIER.
DR	PRINTS: PR00927; ADPTRSLCASE.
DR	PROSITE: PS00215; MITOCH CARRIER. 3.
FT	Mitochondrion; Repeat; Transmembrane; Transport.
FT	NON_TER 288
SEQ	SEQUENCE 288 AA; 31725 MW; 052B0CC005043650 CRC64;

Query Match	77.0%	Score 1187.5	DB 5	length 288
Best Local Similarity	80.7%	Pred. No. 8.6e-101		
Matches 230	Conservative 19	Mismatches 33	Indels 3	Gaps 3

[illegible]

RESULT	11		
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ID	044094	PRELIMINARY:	PRT; 288 AA.
AC	044094:		
DT	01-JUN-1998 (TRENDBEEL. 06		
DT	01-JUN-1998 (TRENDBEEL. 06		
DT	01-OCT-2000 (TRENDBEEL. 15		
DE	ADP/ATP TRANSLOCASE (FRAGMENT).		
EN	SESB.		

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE KOI1H12.2 PROTEIN.
GN KOI1H12.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP Mcmurray A.;
RL Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=94150718; PubMed=7906386;
RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Dublin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Ritken L., Roopra A., Saunders B., Showkneen R.,
RA Shalton L., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlschlag P.;
RT 7.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.".
RT Subcellular location: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
RL Nucle 368.32-38.1(1994).
RL -1- SUPERLOCAL LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC EMBL: Z66218; CAA92472.1; -
DR INTERPRO: IPR001993; -
DR INTERPRO: IPR002067; -
DR INTERPRO: IPR002113; -
DR PFAM: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTNRCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Repeat; Transmembrane; Transport.
QO SEQUENCE 313 AA; 3438 MW; D1E55DDB463C984 CRC64;

[illegible]

Search completed: April 29, 2001, 11:38:54
 Job time: 154 sec

DT 01-MAY-1997 (TReMBLrel. 03, last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, last annotation update)
 DE SIMILAR TO ADP/ATP TRANSLOCASE.
 GN TOB11.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleodermidae; Caenorhabditis.
 NCBI_TaxID=6239.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello J., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hallier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.
 RN Nature 368:32-38(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Stellyes L.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: U080931; AAB38001.1; -
 CC DR INTERPRO: IPR001993; -
 CC DR INTERPRO: IPR002067; -
 CC DR INTERPRO: IPR002113; -
 CC DR PRAM: PF00153; mito_carr; 1.
 CC DR PRINTS: PR00926; MITOCARRIER.
 CC DR PRINTS: PR00927; ADPTRNSLCASE.
 CC DR PROSITE: PS00215; MITOCH CARRIER; 3.
 CC KM Mitochondrion; Repeat: Transmembrane; Transport.
 SQ SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;

Query Match 67.3%; Score 1039; DB 5; Length 313;
 Best Local Similarity 70.9%; Pred. No. 3,9e-87;
 Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;
 QY 8 FAKFLAGGTAIAISKTAAPVIERVKLLLOVQHASKOIADQYKGIIVDCIVIRPKEGV 67
 DB 25 FLIDLAGGTAIAAASVAKTAAPVIERVKLLLOVQDASLTIAADKRYKGIIVDVLRVPEKGY 84
 QY 68 LSPFGRNLANYIRYEPQALNEAFKDKYKQIEFGVDKHPFMRKYPFAGNLASGGAAGTS 127
 DB 85 AALMRGNLANYIRYEPQALNEAFKDKYKQIEFGVDKHPFMRKYPFAGNLASGGAAGTS 144
 QY 128 LCFVYPLDFAFTRLAADVGSKSTEREFRGLDCLVKTFSKDGIRGLYOGFVSVOGIIY 187
 DB 145 LCFVYPLDFAFTRLAADVGSKSTEREFRGLDCLVKTFSKDGIRGLYOGFVSVOGIIY 203
 QY 188 RAAFGYVDTAKGML-PDPKNTIIVSSMTIAQVTAAGVSYPPFTVRRRMMQSGRKG 246
 DB 204 RAAFGYVDTAKGML-PDPKNTIIVSSMTIAQVTAAGVSYPPFTVRRRMMQSGRKG 262
 QY 247 ADIMYTGTVDCWRKIFRDEGSKAFKCGAMSVNLGMDGAPVLYLDELKVI 298
 DB 263 -DVLYKNTLDCAVKIINEGSAMFAGALSINVFRTGALVLAIDEIKFI 313

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 29, 2001, 11:37:06 ; Search time 9.46 Seconds

(without alignments)
1079,084 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQALSFADKLFIAGGIAAA.....LRMGAFVLYDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1	ADT3_HUMAN
2	1512	98.0	298	1	ADT3_BOVIN
3	1463	94.8	298	1	ADT2_HUMAN
4	1451	94.0	298	1	ADT2_RAT
5	1445	93.6	298	1	ADT2_MOUSE
6	1424	92.3	298	1	ADT1_RAT
7	1417	91.8	297	1	ADT1_BOVIN
8	1412	91.5	298	1	ADT1_MOUSE
9	1409	91.3	298	1	ADT1_HUMAN
10	1217.5	78.9	297	1	ADT1_DROME
11	1204	78.0	301	1	ADT1_ANOGA
12	978	63.4	339	1	ADT1_CHLRE
13	778.5	50.5	307	1	ADT3_YEAST
14	772	50.0	308	1	ADT1_CHLRE
15	769	49.8	322	1	ADT1_SCHPO
16	768	49.8	386	1	ADT1_GOSHI
17	766	49.6	313	1	ADT1_NEUCR
18	762.5	49.4	305	1	ADT1_KIULA
19	760.5	49.3	318	1	ADT2_YEAST
20	750	48.6	387	1	ADT1_MAIZE
21	748	48.5	386	1	ADT1_SOLUTU
22	747	48.4	382	1	ADT1_ORYZA
23	744	48.2	387	1	ADT2_MAIZE
24	742.5	48.1	381	1	ADT1_ARATH
25	742.5	48.1	385	1	ADT2_ARATH
26	740	48.0	331	1	ADT1_WHEAT
27	739.5	47.9	386	1	ADT2_SOLUTU
28	737.5	47.8	309	1	ADT1_YEAST
29	727	47.1	331	1	ADT2_WHEAT
30	302	19.6	588	1	CMC2_CAEBL
31	300	19.4	330	1	GDC_BOVIN
32	299	19.4	307	1	YO7L_YEAST
33	297	19.2	587	1	CMC3_CAEBL

34	295	19.1	678	1	CMC1_HUMAN	075746	homo sapien
35	289.5	18.8	322	1	GDC_RAT	P16261	rattus norv
36	287.5	18.6	702	1	CMC1_CAEBL	Q21153	caenorhabdi
37	286	18.5	325	1	BMCP_HUMAN	095258	homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260	homo sapien
39	284	18.4	322	1	BMCP_MOUSE	092282	mus muscicu
40	282.5	18.3	326	1	YE08_SCHPO	013805	schizosacch
41	280	18.1	675	1	CMC2_HUMAN	Q9UJ50	homo sapien
42	265	17.2	312	1	UCP2_HUMAN	P55916	homo sapien
43	265	17.2	676	1	CMC2_MOUSE	09qxx4	mus muscicu
44	265	17.2	695	1	CMC1_DROME	09va73	drosophila
45	264.5	17.1	309	1	UCP2_PIG	097562	sus scrofa

ALIGNMENTS

RESULT	1	ADT3_HUMAN	STANDARD:	PRT:	298 AA.
ID	ADT3_HUMAN				
AC	P12236;				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)				
DE	(ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).				
GN	SLC25A6 OR ANT3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89236396; PubMed=2541251;				
RA	Cozens A.L., Runswick M.J., Walker J.E.;				
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial				
RT	ADP/ATP translocase.";				
RL	J. Mol. Biol. 206:261-280(1989).				
RN	[2]				
RP	SEQUENCE OF 36-298 FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=88124845; PubMed=2829183;				
RA	Houldsworth J., Altardi G.;				
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA				
RT	level in adult human liver.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).				
CC	- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE				
CC	MITOCHONDRIAL INNER MEMBRANE.				
CC	- SUBUNIT: HOMODIMER.				
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL				
CC	INNER MEMBRANE.				
CC	- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
CC	- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL: J03592; AAA36750.1; -				
DR	PIR: S03894; S03894.				
DR	PIR: B28116; B28116.				
DR	MIM: 300151; -				
DR	MIM: 403000; -				
DR	InterPro: IPR001993; -				
DR	InterPro: IPR002067; -				
DR	InterPro: IPR002113; -				
DR	Pfam: PF00153; mito.carr. 1.				
DR	PRINTS: PR00926; MITOCARRIER.				
DR	PRINTS: PR00927; ADPTRNSLCASE.				

DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 105 108 KHTO -> RHA (IN REF. 2).
 SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match 100.0%; Score 1543; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,1e-130;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 |||||
 DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 |||||
 QY 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||||
 DB 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||||
 QY 121 GAAGATSLCFEYPLDFAPATRLAADVGKSGTERERGLDCLVTKSDGIRGLYQGFSSVS 180
 |||||
 DB 121 GAAGATSLCFEYPLDFAPATRLAADVGKSGTERERGLDCLVTKSDGIRGLYQGFSSVS 180
 |||||
 QY 181 VQGITIRAAAFEGYDPAKGLPDPKNTHTIVSMIAQTVAAGVSYSPDVTYRRRMM 240
 |||||
 DB 181 VQGITIRAAAFEGYDPAKGLPDPKNTHTIVSMIAQTVAAGVSYSPDVTYRRRMM 240
 |||||
 QY 241 QSGRKGADIMYTGVDCKRIKFRDEGKAFFKGAMSVNLKMGCAFVLVLYDELKKVI 298
 |||||
 DB 241 QSGRKGADIMYTGVDCKRIKFRDEGKAFFKGAMSVNLKMGCAFVLVLYDELKKVI 298
 |||||

RESULT 2
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 AC P32007;
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DE 01-OCT-2000 (Rel. 40, last annotation update)
 DE ADP/ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLATOR 3) (ANT 3).
 DE SLC25A6 OR ANT3.
 GN Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=69229093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
 RL Biochemistry 28:866-873(1989).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
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 CC -----
 CC EMBL; M24103; AAA30769.1; -;
 DR PIR; B43646; B43646.
 DR InterPro; IPR001993; -;
 DR InterPro; IPR002067; -;
 DR InterPro; IPR002113; -;
 DR Pfam; PF00153; mito_carr; 1.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00927; ADPTNSLOCASE.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 2 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DFE6DE4061 CRC64;

Query Match 98.0%; Score 1512; DB 1; Length 298;
 Best Local Similarity 97.7%; Pred. No. 2,4e-127;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
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 DB 1 MTEQAISFAKDFLAGIAAISTAVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 |||||
 QY 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||||
 DB 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||||
 QY 121 GAAGATSLCFEYPLDFAPATRLAADVGKSGTERERGLDCLVTKSDGIRGLYQGFSSVS 180
 |||||
 DB 121 GAAGATSLCFEYPLDFAPATRLAADVGKSGTERERGLDCLVTKSDGIRGLYQGFSSVS 180
 |||||
 QY 181 VQGITIRAAAFEGYDPAKGLPDPKNTHTIVSMIAQTVAAGVSYSPDVTYRRRMM 240
 |||||
 DB 181 VQGITIRAAAFEGYDPAKGLPDPKNTHTIVSMIAQTVAAGVSYSPDVTYRRRMM 240
 |||||
 QY 241 QSGRKGADIMYTGVDCKRIKFRDEGKAFFKGAMSVNLKMGCAFVLVLYDELKKVI 298
 |||||
 DB 241 QSGRKGADIMYTGVDCKRIKFRDEGKAFFKGAMSVNLKMGCAFVLVLYDELKKVI 298
 |||||

RESULT 3
 ADT2_HUMAN STANDARD; PRT; 298 AA.
 AC P05141; O43350;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-OCT-1994 (Rel. 30, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE ADP/ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2) (ADENINE NUCLEOTIDE TRANSLATOR 2) (ANT 2).
 DE SLC25A5 OR ANT2.
 GN Homo sapiens (human).
 OS Homo sapiens (human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90375457; PubMed=2166878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;

RT "The human fibroblast adenine nucleotide translocator gene. Molecular cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87166056; PubMed=3031073;
 RA Battisti R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
 Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraia R.,
 Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozersky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----
 DR EMBL: M57424; AAA51737.1; -;
 DR EMBL: J02683; AAA55579.1; -;
 DR EMBL: L78810; AAB39266.1; -;
 DR EMBL: AC004000; AAB96347.1; -;
 DR EMBL: J03591; AAA36749.1; -;
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR MIM: 300150; -;
 DR InterPro: IPR001993; -;
 DR InterPro: IPR002067; -;
 DR InterPro: IPR002113; -;
 DR Pfam: PF00153; mito_carr.1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLASE.
 DR PROSITE: PS00215; MITOCH_CARRIER.3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).

FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;
 Query Match 94.8%, Score 1463; DB 1; Length 298;
 Best Local Similarity 92.9%; Pred. No. 5.4e-123;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 OY 1 MTEQATSFRAKPEFLAGGIAAATSKTAVAPLERKLLLOVQHASKQIAAKQKGYDLCIVR 60
 DB 1 MTDAAVSFAKDFLAGGVAASIKSTAVAPLERKLLLOVQHASKQIYADKQKGIIDCVVR 60
 OY 61 IPKEGVLSFPMGNLANIYRFPYTOALNFAFKDKYKQIFLGGVDHNTQFMWFAAGNLASG 120
 DB 61 IPKEGVLSFPMGNLANIYRFPYTOALNFAFKDKYKQIFLGGVDHNTQFMWFAAGNLASG 120
 OY 121 GAAGATSLCFYVPLDFATRLAADYKSGTEREPGLDCLVKITKSGICGLYGFSSVS 180
 DB 121 GAAGATSLCFYVPLDFATRLAADYKSGTEREPGLDCLVKITKSGICGLYGFSSVS 180
 OY 161 VGGITTYRAAYFGVYDPAKGMIPDKNTHIVSMIAQTVAVAGVSPDPTVRRMM 240
 DB 161 VGGITTYRAAYFGVYDPAKGMIPDKNTHIVSMIAQTVAVAGVSPDPTVRRMM 240
 OY 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKGAANSVLKMGCAFVLVLDLKK 296
 DB 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKGAANSVLKMGCAFVLVLDLKK 296
 RESULT 4
 ADT2_RAT STANDARD; PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ADP/ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
 DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinozawa Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----
 DR EMBL: D12771; BA02238.1; -;
 DR InterPro: IPR001993; -;
 DR InterPro: IPR002067; -;
 DR InterPro: IPR002113; -;

DR	Pfam: PF00153; mito_carr: 1.
DR	PRINTS: PR00926; MITOCARRIER.
DR	PROSITE: PRO0927; ADPTRSLCASE.
DR	PROSITE: PS00215; MITOCH_CARRIER: 3.
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW	MultiGene family.
RK	TRANSMEM 12 29 1 (POTENTIAL).
FT	TRANSMEM 73 91 2 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 214 231 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 1 111 1.
FT	REPEAT 112 208 2.
FT	REPEAT 209 298 3.
SO	SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;
<hr/>	
Query Match	94.0%; Score 1451; DB 1; Length 298;
Best Local Similarity	91.9%; Pred. No. 6.3e-122;
Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;	
QY	1 MTEQAISFAKDFLAGGIAAISKTAVAPIERKLLQVOHASKQIADAKOYKGIIVDCIVR 60
Dd	1 MTDAVSPFAKDLPLAGVAALASKTAVAPIERKLLQVOHASKQITADKQYGIIDCVRR 60
QY	61 IPKEGVLSIFWRGNLANRYIRFPYQALNFAEKDKYKKQIFLGVDGKHQOFWRYPAGNLASG 120
Dd	61 IPEKGVLSEFWRGNLANRYIRFPYQALNFAEKDKYKKQIFLGVDGRKTOFWRFAPAGNLASG 120
QY	121 GAAGATSLCPFYPLDFAFRTRLAADVGSKSTEEFEFGLDGCIVTKIKSGICRGLYOGFSVS 180
Dd	121 GAAGATSLCFEYPLDFAFRTRLAADVGKAAGEREFGLDCLVIKYKSIGLGYGFNVSS 180
QY	181 VGGIIIEAAAFEGVYDTAKGMLPDKNHIYVSWMIADTVTAVAGVSYPFDVRRMM 240
Dd	181 VGGIIIEAAAFEGVIDTAKGMPLDPKNHIIFLSMIIASVTAVAAILTSFEPFTVRRMM 240
QY	241 QSGRKGDIMYTGTIVDCNRKIIFRDGGAFFKFGANSVLRNGGAFFVLVYLDELKK 296
Dd	241 QSGRKGTIDMYTGTLDCWRKIARDEGGAFFKFGANSVLRMGGAFFVLVLYDEIKK 296
<hr/>	
RESULT 5	
ID	ADT2_MOUSE STANDARD; PRT; 298 AA.
AC	P51881; Q61311;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	ADP, ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DN	(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RC	TISSUE=Skeletal muscle;
RA	Sheldon J.G.;
RL	Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT	"Rapid evolution of human pseudautosomal genes and their mouse
RT	homologs.";
RL	Mamm. Genome 7:25-30(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skeletal muscle;
RA	Sheldon J.G.;
RL	Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT	"Rapid evolution of human pseudautosomal genes and their mouse
RT	homologs.";
RL	Mamm. Genome 7:25-30(1996).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skeletal muscle;
RA	Sheldon J.G.;
RL	Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT	"Rapid evolution of human pseudautosomal genes and their mouse
RT	homologs.";
RL	Mamm. Genome 7:25-30(1996).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skeletal muscle;
RA	Sheldon J.G.;
RL	Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT	"Rapid evolution of human pseudautosomal genes and their mouse
RT	homologs.";
RL	Mamm. Genome 7:25-30(1996).

Query Match	Best Local Similarity	91.6%	Score 1445;	DB 1;	Length 298;
Matches 271;	Conservative 15;	Mismatches 10;	Indels 0;	Gaps 0;	
QY 1 MTEQALSPFAKPEFLNAGGIAAISTKTAIVAPIEYKLLDLYQVHASKQIAODKQYKGIIVDCIVR 60	1	1	1	1	1
Db 1 MTDAAVSPRAKQFLAGGVAALAIKTAIVAPIERVKLLDLYQVHASKQIOTADKQYKGIIDCVRR 60	1	1	1	1	1
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGGVDKHHQFWRYEAGNLASG 120	61	1	1	1	1
Db 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGGVDKHHQFWRYEAGNLASG 120	61	1	1	1	1
QY 121 GAACATSLCEFYYPIDFATRIAAVYKSGKTERFERRGDCLVYKITSKSGISGLYQGFVS 180	121	1	1	1	1
Db 121 GAACATSLCEFYYPIDFATRIAAVYKSGKTERFERRGDCLVYKITSKSGISGLYQGFVS 180	121	1	1	1	1
QY 181 VQGIITVFAAEEYGVDPFKGMLPDKNTHIVYNNIAQTVTAIVAGVSYPPDVTARRMM 240	181	1	1	1	1
Db 181 VQGIITVFAAEEYGVDPFKGMLPDKNTHIVYNNIAQTVTAIVAGVSYPPDVTARRMM 240	181	1	1	1	1
QY 241 QSGRGKADIMVTGTVDKWRKIFRDEGGKAFKFGKAMSVNLRMGGAFLVLYDELK 296	241	1	1	1	1
Db 241 QSGRGKADIMVTGTVDKWRKIFRDEGGKAFKFGKAMSVNLRMGGAFLVLYDELK 296	241	1	1	1	1

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ADT1_RAT
ID ADT1_RAT STANDARD: PRT: 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLIC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY, AND WISTAR: TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kanada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator";
RL Biochem. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X61667; CAA3842.1; -
DR EMBL: D12770; BAA02237.1; -
DR InterPro: IPR001993; -
DR InterPro: IPR002067; -
DR InterPro: IPR002113; -
DR Pfam: PF00153; mito_carr.1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;
Query Match 92.3%; Score 1424; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.6e-119;
Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
OY 1 MTEQAISFAKDPDLAGGIAAISTKAVPIERKLLQVOHASKQIAADKQYGIYDCIYR 60
DB 1 MGDQALSLFKDLPLAGGIAAASKTAVPIERKLLQVOHASKQIAAEOYGIYDCIYR 60
OY 61 IPEEGVLSFWRGNTLVNIRYPTQALNFAFKDKTKQKFLGVDKXHTQFWRYPAGNLSAG 120
DB 61 IPEEGVLSFWRGNTLVNIRYPTQALNFAFKDKTKQKFLGVDKXHTQFWRYPAGNLSAG 120

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OY 121 GAAGATSLCFVYPLDFARTRLADYKSGTGEREFGLDCLVKITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADYKSGTGEREFGLDCLVKITKSDGIRGLYOGFSVS 180
OY 181 VGGIITRYAAVFGVYDTAKGMLPDKPNHIVYSNMIAOTVAVAGVSPEDTVRRMM 240
DB 181 VGGIITRYAAVFGVYDTAKGMLPDKPNHIVYSNMIAOSVPAVLAVSPEDTVRRMM 240
OY 241 OSGRGADIMVTGVDCAKRIERDEGKAFKFGAASNVLRGMAFVLYVDELKKYI 298
DB 241 OSGRGADIMVTGVDCAKRIERDEGKAFKFGAASNVLRGMAFVLYVDELKKYI 298

RESULT 7
ADT1_BOVIN
ID ADT1_BOVIN STANDARD: PRT: 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE 1)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLIC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RC MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OE 207-297 FROM N.A.
RC MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
RN [4]
RP FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
RP MITOCHONDRIAL INNER MEMBRANE.
RP -1- SUBUNIT: HOMODIMER.
RP -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
RP INNER MEMBRANE.
RP -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
RP -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
RP -----
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RP use by non-profit institutions as long as its content is in no way
RP modified and this statement is not removed. Usage by and for commercial
RP entities requires a license agreement (see http://www.isb-sib.ch/announce/
RP or send an email to license@isb-sib.ch).
RP -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A03181; XMBO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR001993; -
DR InterPro: IPR002067; -

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DR InterPro: IPR002113; -
DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW MultiGene family; Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3CA4A0AE848 CRC64;

Query Match 91.8%; Score 1417; DB 1; Length 297;
Best Local Similarity 89.2%; Pred. No. 6.6e-119;
Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 2 TEQATSFAPKDFLAGIAAISTAVAPIERVKLLQVQHSKQIADKQYGIYDCIYRI 61
   1 SDQALSFLLKDFLAGVAAIAISTAVAPIERVKLLQVQHSKQIADKQYGIYDCIYRI 60
Db 1 SDQALSFLLKDFLAGVAAIAISTAVAPIERVKLLQVQHSKQIADKQYGIYDCIYRI 60
QY 62 PKEGCVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGG 121
   61 PKEGCVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGG 120
Db 61 PKEGCVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGG 120
QY 122 AAGATSLCFEYVPLDPAFRLADVGKSGTEREFGJGDCIVKTFKSDGIRGLYQGFSSVS 181
   121 AAGATSLCFEYVPLDPAFRLADVGKGAQREFTGLGNCITKIFKSDGLRGLYQGFSSVS 180
Db 121 AAGATSLCFEYVPLDPAFRLADVGKGAQREFTGLGNCITKIFKSDGLRGLYQGFSSVS 180
QY 182 QGIIYRAAYFGVYDTAKGMLPDPKNTIIVYSWMIQTQVTVAVGVSYPPDTVRRMMQ 241
   181 QGIIYRAAYFGVYDTAKGMLPDPKNTIIVYSWMIQTQVTVAVGVSYPPDTVRRMMQ 240
Db 181 QGIIYRAAYFGVYDTAKGMLPDPKNTIIVYSWMIQTQVTVAVGVSYPPDTVRRMMQ 240
QY 242 SGRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNTLRMGGAFLVLYDELKVIY 298
   241 SGRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNTLRMGGAFLVLYDEIKKVF 297
Db 241 SGRKADIMYTGTVDCWRKIFRDEGKAFKFGAMSNTLRMGGAFLVLYDEIKKVF 297

RESULT 8
ADT1_MOUSE STANDARD; PRT; 298 AA.
AC P48962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

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CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27315; AAC52837.1; -
DR MGD: MGI:1353495; SLC25a4.
DR InterPro: IPR001993; -
DR InterPro: IPR002067; -
DR InterPro: IPR002113; -
DR Pfam: PF00153; mito_carr; 1.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW MultiGene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32870 MW; 3ZAC3BAEFCFA482 CRC64;

Query Match 91.5%; Score 1412; DB 1; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.9e-118;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQATSFAPKDFLAGIAAISTAVAPIERVKLLQVQHSKQIADKQYGIYDCIYRI 60
   1 MGDQALSFLLKDFLAGVAAIAISTAVAPIERVKLLQVQHSKQIADKQYGIYDCIYRI 60
Db 1 MGDQALSFLLKDFLAGVAAIAISTAVAPIERVKLLQVQHSKQIADKQYGIYDCIYRI 60
QY 61 PKEGCVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
   61 IPKEGCVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
Db 61 IPKEGCVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFEYVPLDPAFRLADVGKSGTEREFGJGDCIVKTFKSDGIRGLYQGFSSVS 180
   121 GAAGATSLCFEYVPLDPAFRLADVGKSSQREFNGJGDCITKIFKSDGLKGLYQGFSSVS 180
Db 121 GAAGATSLCFEYVPLDPAFRLADVGKSSQREFNGJGDCITKIFKSDGLKGLYQGFSSVS 180
QY 181 VOGIIYRAAYFGVYDTAKGMLPDPKNTIIVYSWMIQTQVTVAVGVSYPPDTVRRMMQ 240
   181 VOGIIYRAAYFGVYDTAKGMLPDPKNTIIVYSWMIQTQVTVAVGVSYPPDTVRRMMQ 240
Db 181 VOGIIYRAAYFGVYDTAKGMLPDPKNTIIVYSWMIQTQVTVAVGVSYPPDTVRRMMQ 240
QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSNTLRMGGAFLVLYDELKVIY 298
   241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSNTLRMGGAFLVLYDEIKKVF 298
Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSNTLRMGGAFLVLYDEIKKVF 298

RESULT 9
ADT1_HUMAN STANDARD; PRT; 298 AA.
AC P12235;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89236396; PubMed=2541251;
RA	Cozens A.L., Runswick M.J., Walker J.E.;
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial
RT	ADP/ATP translocase.";
RL	J. Mol. Biol. 206:261-280(1989).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89340499; PubMed=2547778;
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA	Fukuyama R., Meekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT	"A human muscle adenine nucleotide translocator gene has four exons,
RT	is located on chromosome 4, and is differentially expressed.";
RL	J. Biol. Chem. 264:13998-14004(1989).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=88041149; PubMed=2823266;
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RA	Reckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT	"DNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT	of a leader peptide, divergence from a fibroblast translocator cDNA,
RT	and coevolution with mitochondrial DNA genes.";
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN	[4]
RP	SEQUENCE OF 1-37 FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=88124845; PubMed=2829183;
RA	Houldsworth J., Attardi G.;
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT	level in adult human liver.";
RL	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC	MITOCHONDRIAL INNER MEMBRANE.
CC	-1- SUBUNIT: HOMODIMER.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC	INNER MEMBRANE.
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; J02966; AAA61223.1; -
DR	EMBL; J03593; AAA36751.1; -
DR	EMBL; J04982; AAA51736.1; -
DR	PIR; A28116; A28116.
DR	PIR; A39891; A39891.
DR	PIR; S03893; S03893.
DR	PIR; A44778; A44778.
DR	MIM; 103320; -
DR	InterPro: IPR001993; -
DR	InterPro: IPR002067; -
DR	InterPro: IPR002113; -
DR	InterPro: IPR002113; -
DR	pfam: PF00153; mito_carr; 1.
DR	PRINTS; PR00926; MITOCARRIER.
DR	PRINTS; PR00927; ADPTNSLCASE.
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW	Mitogenic family.
FT	TRANSMEM 12 29 1 (POTENTIAL).
FT	TRANSMEM 73 91 2 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 214 231 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 1 110 1.
FT	REPEAT 111 208 2.

FT	REPEAT	209	298	3	G -> A (IN REF. 3).
FT	CONFLICT	16	16		KGA -> RR (IN REF. 3).
FT	CONFLICT	147	149		V -> L (IN REF. 3).
FT	CONFLICT	227	227		
SO	SEQUENCE	298 AA:	33064 MM:	59F0DFACCA4ETCEBB	CRC64:

Query Match	91.3%:	Score 1409:	DB 1:	Length 298:
Best Local Similarity	88.3%:	Pred. No. 3.4e-118:		
Matches 263:	Conservative 19:	Mismatches 16:	Indels 0:	Gaps

Qy	1	MTEBAISPAKQFLAGGIAAISTKTAVAPIREVKLLILOVHAHSKIOADKQKGIIVDCIVR	60
Db	1	MGDHAWSPLEKDFLAGVAAAASKTAVAPIREVKLLILOVHAHSKIOASAKOTKGIIDCVR	60
Qy	61	IPKRGVLSFEMRGMLANVIRIFPTQALNFAFKDKYKQIFLAGVGNKHQFMRFAGNLSG	120
Db	61	IPKRGGLSFEMRGMLANVIRIFPTQALNFAFKDKYKQIFLAGVGNKHQFMRFAGNLSG	120
Qy	121	GAGATSLCFEYVPLDFAFTRLADVGSKGEREFERGLDCLVTKTSDGIRGLYOGFSVS	180
Db	121	GAGATSLCFEYVPLDFAFTRLADVGSKGAQREFRHGLDCLIKTFKSDGLGLYOGFNVS	180
Qy	181	VOGIIITRAAEFGYVDPAKGLPDKPKNTHIVSMIAQOTVAVGVVSYPRDTVRRMM	240
Db	181	VOGIIITRAAEFGYVDPAKGLPDKPKNTHIVSMIAQOTVAVGVVSYPRDTVRRMM	240
Qy	241	QSGRRGADIMYTGIVDCWRKIFPRDEGKAPFKGAMSVNLRMGCAFVLVLYDELKVI	298
Db	241	QSGRRGADIMYTGIVDCWRKIRAKDEGKAPFKGAMSVNLRMGCAFVLVLYDELKVI	298

RESULT 10	ADT_DROME	STANDARD:	PRT:	297 AA.
ADT_DROME				
IC	ADT_DROME	STANDARD:	PRT:	297 AA.
AC	026365:	026254:	P91614:	Q9VZ70:
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLUCASE) (ADENINE NUCLEOTIDE TRANSLUCATOR) (ANT) (SPRESS SENSITIVE B PROTEIN).			
CN	SESB OR A/A-T OR CG16944.			
OC	Drosophila melanogaster (fruit fly).			
OC	Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:			
OC	Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:			
OC	Ephydroidea: Drosophilidae: Drosophila.			
OX	NCBI_TaxID=7227:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92389367:	PubMed=1387687:		
RA	Louvi A., Tstiliou S.G.:			
RT	"A cDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases."			
RL	J. Mol. Evol. 35:44-50(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94350065:	PubMed=7520869:		
RA	Hutter P., Karch F.:			
RT	"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila."			
RL	Experientia 50:749-762(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-OREGON-R.			
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.:			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-BERKELEY:			
RX	MEDLINE=20196005:	PubMed=10731132:		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			

DR InterPro: IPR002067; -
 DR InterPro: IPR002113; -
 DR Pfam: PF00153; mito_carr: 1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER, 3.
 DR MitoChondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;
 Best Local Similarity 77.7%; Pred. No. 6e-100;
 Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

QY 1 MTEGAD--ISFAKDFLAGGIAAISTAVAPIERVKLLQVHASKQIADKQYKGVDCI 58
 DB 1 MTKKADPYGFAKDFLAGGISAANVSKTAVAPIERVKLLQVHASKQIADKQYKGVDCI 60
 QY 59 VRIPEGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 118
 DB 61 VRIPEGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 120
 QY 119 SGGAAGATSLCFVYPLDPARTRLADYKSGTEREFGGLDCLVTKTSKDIKGLYQGS 178
 DB 121 SGGAAGATSLCFVYPLDPARTRLADYKSGTEREFGGLDCLVTKTSKDIKGLYQGS 180
 QY 179 VSVGGIITIRAYRGVYDPAKGLPDPKNTIIVSMMIAQVTVAVAGVSYFPTVRRRM 238
 DB 181 VSVGGIITIRAYRGVYDPAKGLPDPKNTIIVSMMIAQVTVAVAGVSYFPTVRRRM 240
 QY 239 MMSGKRGADIMYTGVDCKRIFRDEGKAFFKGAWSNVLRGMAFVLYDELKVI 298
 DB 241 MMSGKRGADIMYTGVDCKRIFRDEGKAFFKGAWSNVLRGMAFVLYDELKVI 300

RESULT 12
 ADT_CHLKE STANDARD; PRT; 339 AA.
 AC P1692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
 DE TRANSLOCATOR) (ANT).
 DE Chlorella keesleri.
 OS Chlorella keesleri.
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorella.
 OC NCBI_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084708; PubMed=1748677;
 RA Hilgarch C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the
 RT glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC -----

DR EMBL: M76669; AAA33027.1; -
 DR PIR: A41677; A41677.
 DR InterPro: IPR001993; -
 DR InterPro: IPR002067; -
 DR InterPro: IPR002113; -
 DR Pfam: PF00153; mito_carr: 1.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER, 3.
 DR MitoChondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A3B3942 CRC64;

Query Match 63.4%; Score 978; DB 1; Length 339;
 Best Local Similarity 66.9%; Pred. No. 8.6e-80;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISFAKDFLAGGIAAISTAVAPIERVKLLQVHASKQIADK--QYKGVDCIIRIPK 63
 DB 39 MAFVKDLAAGTAAIGSTAVAPIERVKLLQVHASKQIADK--QYKGVDCIIRIPK 98
 QY 64 EGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 123
 DB 99 EGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 157
 QY 124 GATSLCFVYPLDPARTRLADYKSGTEREFGGLDCLVTKTSKDIKGLYQGS 183
 DB 158 GATSLCFVYPLDPARTRLADYKSGTEREFGGLDCLVTKTSKDIKGLYQGS 216
 QY 184 IIVIRGAVFGIYDPAKGLPDPKNTIIVSMMIAQVTVAVAGVSYFPTVRRRM 242
 DB 217 IIVIRGAVFGIYDPAKGLPDPKNTIIVSMMIAQVTVAVAGVSYFPTVRRRM 276
 QY 243 GRKGADIMYTGVDCKRIFRDEGKAFFKGAWSNVLRGMAFVLYDELKVI 298
 DB 277 --GGERQYNGTIDCKRKVAQOEGKKAFFKGAWSNVLRGMAFVLYDELKVI 329

RESULT 13
 ADT3_YEAST STANDARD; PRT; 307 AA.
 AC P18238;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP,ATP CARRIER PROTEIN 3 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE
 DE TRANSLOCATOR 3) (ANT 3).
 DE AAC3 OR YBR085W OR YBR0753.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90324269; PubMed=2165073;
 RA Kolarov J., Kolarova N., Nelson N.;
 RT "A third ADP/ATP translocator gene in yeast.";
 RL J. Biol. Chem. 265:12711-12716(1990).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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Db 239 RRMWTS---GSAYKYNSSFFHCEIIVKNEGMKSLFKGAGANILRAVAGAGVAGYDOLQ 295
 QY 296 KVI 298
 Db 296 VIL 298

RESULT 15

ADT_SCHPO STANDARD; PRT; 322 AA.

AC 009188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ADP_CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
 TRANSLOCATOR) (ANT).
 GN ANCI OR SPEC530.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
 carrier of Schizosaccharomyces pombe by functional complementation in
 RT Saccharomyces cerevisiae.";
 RL Gene 171:113-117(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC
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 CC
 CC EMBL; Z49974; CAA90275.1; -
 CC EMBL; AL023634; CAA19176.1; -
 DR HSSP; P04002; IATF.
 DR InterPro: IPR001993; -
 DR InterPro: IPR002067; -
 DR InterPro: IPR002113; -
 DR Pfam; PF00153; mito_carr; 1.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00927; ADPTRNSLCASE.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;

Query Match 49.8%; Score 769; DB 1; Length 322;
 Best Local Similarity 53.6%; Pred. No. 3,2e-61;
 Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps 6;

QY 7 SFADFLAGIAAIAIKTAVAPIERVKLLLOVHASKIOADK---QYKGIVDICIVRPK 63
 Db 26 TFFDFEMMGVSAVSKTAAPIERVKLLIQNQ--DEMIRAGRSLSHRYKIGCECFKRTAA 83
 QY 64 EGVLSFWRGNLIANYIRYFPQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGAA 123
 Db 84 EGVLSLWRGNTAVNLRFFPQALNFAFKDKFKME--GKNERDGYAKMFPAGNLASGAA 142
 QY 124 GATSLCFVYPLDFAFTRLADY--GKSGTEREPFRLGDLVYKTSQDIRGLYQGFVSV 181
 Db 143 GAASLLEFVSLDYATRLANDAKSAKKGGERQFNGLVYVRYKTYRSDGLRGLYRQGFPSV 202
 QY 182 QGIIIRAAVFGVVDLAG--MLPDPKNTIYVSMIAOTYAVAGVYSYPPDYARRRMM 240
 Db 203 VGIIVYRGLYRGMDTLKPVYLVGPLEGNFLASFLGVAVTGSGVASYPLDTIRRRMM 262
 QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPGKAGMSVLRMGAFVLYVDELK 295
 Db 263 TSGEA---VKYSSFEQGRQILAKEGARSPFKGAGANILRGVAGAGVSTYDQV 314

Search completed: April 29, 2001, 11:39:14
 Job time: 128 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 29, 2001, 11:35:45 ; Search time 16.58 seconds
(without alignments)
1235.189 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543

Sequence: 1 MTEQAIISFAKDFLAGGIAA.....LRMGGAFLVLYDELKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_67:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	1 S03894	ADP,ATP carrier pr
2	1512	98.0	298	1 B43646	ADP,ATP carrier pr
3	1454	94.2	298	1 A29132	ADP,ATP carrier pr
4	1424	92.3	298	1 T60173	adenine nucleotide
5	1422	92.2	298	1 XWBO	ADP,ATP carrier pr
6	1418	91.9	298	1 S37210	ADP,ATP carrier pr
7	1409	91.3	298	1 A44778	ADP,ATP carrier pr
8	1405	91.1	298	1 S31814	ADP,ATP carrier pr
9	1184	76.7	301	1 S31935	ADP,ATP carrier pr
10	1041	67.5	313	1 T23207	hypothetical prote
11	1039	67.3	313	1 T25850	hypothetical prote
12	1038	67.3	300	1 T25371	hypothetical prote
13	993.5	64.4	300	1 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP,ATP carrier pr
15	943	61.1	301	2 S51132	ADP,ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP,ATP carrier pr
17	772	50.0	308	1 S30259	ADP,ATP carrier pr
18	769	49.8	322	2 T40526	ADP,ATP translocas
19	768	49.8	386	2 T09709	ADP,ATP carrier pr
20	766	49.6	313	1 XWNC	ADP,ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP,ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP,ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14876	ADP,ATP carrier pr
26	748	48.5	386	2 S21974	ADP,ATP carrier pr
27	747	48.4	306	2 T42011	ADP,ATP carrier pr
28	747	48.4	386	2 S17917	ADP,ATP carrier pr
29	744	48.2	387	2 S16568	ADP,ATP carrier pr

30	743	48.2	379	2 T04608	ADP,ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP,ATP carrier pr
32	742	48.1	382	2 S33630	ADP,ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP,ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP,ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP,ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP,ATP translocas
38	383	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	mitochondrial solu
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	344.5	22.3	332	2 T47703	Ca-dependent solut
45	321.5	20.8	479	2 T49871	peroxisomal Ca-dep

ALIGNMENTS

RESULT 1
S03894
ADP,ATP carrier protein T3 - human
N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
R:Accession: S03894; B28116
R:Cozens, A.L., Runswick, M.J., Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396
A:Accession: S03894
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HO2>
A:Cross-references: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT3; ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <ANT>
F:3-99/Domains: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domains: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domains: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.4e-129;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MTEQAIISFAKDFLAGGIAAISKTAVERKLLQVQHASKOIAADKOKYGVDCIVR	60
Db	1	MTEQAIISFAKDFLAGGIAAISKTAVERKLLQVQHASKOIAADKOKYGVDCIVR	60
Oy	61	IPKEGVLSFMRGNLANVIRFPQALNFAKDKYKQIFLGVGVDKHTQFMRYPAGNLASG	120
Db	61	IPKEGVLSFMRGNLANVIRFPQALNFAKDKYKQIFLGVGVDKHTQFMRYPAGNLASG	120
Oy	121	GAAGATSLCFYVPLDFATRLAADVGKSTGEREPGLDCLVKTIKSGISGLVQGFSSVS	180
Db	121	GAAGATSLCFYVPLDFATRLAADVGKSTGEREPGLDCLVKTIKSGISGLVQGFSSVS	180

QY 181 VGGIIIVRAAFGVYDTRAKGMLPDPKNTNTHIVSMIAQTVAAGVSYPEPTVRRMM 240
 |||||||
 Db 181 VGGIIIVRAAFGVYDTRAKGMLPDPKNTNTHIVSMIAQTVAAGVSYPEPTVRRMM 240
 |||||||

QY 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||
 Db 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||

RESULT 2

B43646
 ADP/ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match Best Local Similarity 98.0%; Score 1512; DB 2; Length 298;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISTKTAVAPIERVKLLQVQHSKQIADKQYKGIIVDCIVR 60
 |||||||
 Db 1 MTEQAISFAKDFLAGGIAAISTKTAVAPIERVKLLQVQHSKQIADKQYKGIIVDCIVR 60
 |||||||

QY 61 IPKQGVLSFMRGMLNANIRFPPQALNFAFKDKYKQIFLGGVNDKHQFMFRFAGNLASG 120
 |||||||
 Db 61 IPKQGVLSFMRGMLNANIRFPPQALNFAFKDKYKQIFLGGVNDKHQFMFRFAGNLASG 120
 |||||||

QY 121 GAAGATSLCFEYPLDPFARTRIAAADVKGSGTEREFGJLDDCLVTKTSGDITGLVQGFSSV 180
 |||||||
 Db 121 GAAGATSLCFEYPLDPFARTRIAAADVKGSGTEREFGJLDDCLVTKTSGDITGLVQGFSSV 180
 |||||||

QY 181 VGGIIIVRAAFGVYDTRAKGMLPDPKNTNTHIVSMIAQTVAAGVSYPEPTVRRMM 240
 |||||||
 Db 181 VGGIIIVRAAFGVYDTRAKGMLPDPKNTNTHIVSMIAQTVAAGVSYPEPTVRRMM 240
 |||||||

QY 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||
 Db 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||

RESULT 3

A29132
 ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Batlini, R.; Ferrali, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 267, 4355-4359, 1992
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87160056
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Houldsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'U', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:

A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match Best Local Similarity 94.2%; Score 1454; DB 1; Length 298;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISTKTAVAPIERVKLLQVQHSKQIADKQYKGIIVDCIVR 60
 |||||||
 Db 1 MTEQAISFAKDFLAGGIAAISTKTAVAPIERVKLLQVQHSKQIADKQYKGIIVDCIVR 60
 |||||||

QY 61 IPKQGVLSFMRGMLNANIRFPPQALNFAFKDKYKQIFLGGVNDKHQFMFRFAGNLASG 120
 |||||||
 Db 61 IPKQGVLSFMRGMLNANIRFPPQALNFAFKDKYKQIFLGGVNDKHQFMFRFAGNLASG 120
 |||||||

QY 121 GAAGATSLCFEYPLDPFARTRIAAADVKGSGTEREFGJLDDCLVTKTSGDITGLVQGFSSV 180
 |||||||
 Db 121 GAAGATSLCFEYPLDPFARTRIAAADVKGSGTEREFGJLDDCLVTKTSGDITGLVQGFSSV 180
 |||||||

QY 181 VGGIIIVRAAFGVYDTRAKGMLPDPKNTNTHIVSMIAQTVAAGVSYPEPTVRRMM 240
 |||||||
 Db 181 VGGIIIVRAAFGVYDTRAKGMLPDPKNTNTHIVSMIAQTVAAGVSYPEPTVRRMM 240
 |||||||

QY 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||
 Db 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKVI 298
 |||||||

RESULT 4

160173
 adenine nucleotide translocator - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: 160173
 R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: 160173; MUID:94002161
 A:Accession: 160173
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
 C:Genetics:
 A:Gene: antl
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match Best Local Similarity 92.3%; Score 1424; DB 2; Length 298;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 1 MGDQALSLKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 Db 1 MGDQALSLKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 Db 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 QY 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPEDTVRRMM 240
 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPEDTVRRMM 240
 Db 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPEDTVRRMM 240
 QY 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFFKGAWSNVLKRGCAFVLVLYDELKVI 298
 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFFKGAWSNVLKRGCAFVLVLYDELKVI 298
 Db 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFFKGAWSNVLKRGCAFVLVLYDELKVI 298

RESULT 5

XMBQ

ADP, ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:8922093
 A:Accession: A43646

A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
 R:Rasmussen, U.B.; Wohlrab, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:8629575
 A:Accession: A24822

A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Mista, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82188267
 A:Accession: A03181

A:Molecule type: protein
 A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AQU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A61343; MUID:82046808
 A:Accession: A61343

A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetle, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-7-azido-4-isopropyladenosine labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:95172058
 A:Accession: S69369

A:Molecule type: protein
 A:Residues: 49-63; 154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondria
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mito
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;
 Best Local Similarity 89.3%; Pred. No. 7.1e-118;
 Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 1 MSDQALSLKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 Db 1 MSDQALSLKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 Db 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 QY 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPEDTVRRMM 240
 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPEDTVRRMM 240
 Db 181 VOGIITVRAAFYGVYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPEDTVRRMM 240
 QY 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFFKGAWSNVLKRGCAFVLVLYDELKVI 298
 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFFKGAWSNVLKRGCAFVLVLYDELKVI 298
 Db 241 OSGRKGADIMYTGIVDCMRKIFRDEGKAFFKGAWSNVLKRGCAFVLVLYDELKVI 298

RESULT 6

S37210

ADP, ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Laplace, C.; Costet, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210

A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 1-298 <LAP>
 A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
 C:Genetics:
 A:Gene: ANCI

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.9%; Score 1418; DB 2; Length 298;
 Best Local Similarity 88.9%; Pred. No. 7.1e-118;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 1 MGDQALSLKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 Db 1 MGDQALSLKDFLAGGIAAISKTAAPIERVKLLQVQHASKOJAADKQKGIYDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 Db 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRFPAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180
 Db 121 GAAGATSLCFEYPLDFAFTRILAADVGKSGTEREPFGLDCLVKITKSGIGLYOGFSVS 180

QY 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTIVSWMIAQTAVAGVSYPPDVTYRRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTIVSWMIAQTAVAGVSYPPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGVDWCWKIFRDEGKAFKFGAMSVNLKMGAFVLYLYDELKVI 298
 Db 241 QSGRKGADIMYTGVDWCWKIFRDEGKAFKFGAMSVNLKMGAFVLYLYDELKVI 298

RESULT 7

A44778
 ADP/ATP carrier protein T1 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 1
 C:Species: Homo sapiens (man)
 C>Date: 17-Mar-2000 #sequence-revision 17-Mar-2000 #text-change 17-Mar-2000
 C:Accession: A44778; S03893; A39891; A28116
 R:Li, K.; Warner, C.K.; Hodge, J.B.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.; J. Biol. Chem. 264, 13998-14004, 1989
 A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
 A:Reference number: A44778; MUID:89340499
 A:Accession: A44778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-298 <LTA>
 A:Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659
 R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989
 A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
 A:Reference number: S03893; MUID:99236396
 A:Accession: S03893
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-298 <COZ>
 R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
 A:Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader
 A:Reference number: A39891; MUID:88041149
 A:Accession: A39891
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
 A:Cross-references: GB:J02366; NID:g339919; PIDN:AAA61223.1; PID:g339920
 A:Experimental source: clone pMAN7
 R:Houlsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
 A:Reference number: A94197; MUID:86124845
 A:Accession: A28116
 A:Molecule type: mRNA
 A:Residues: 1-37 <HO>
 A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725
 A:Experimental source: liver
 C:Genetics:
 A:Gene: GDB:ANF1; T1
 A:Cross-references: GDB:119680; OMIM:103220
 A:Map position: 4q35-4q35
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;
 Best Local Similarity 88.3%; Pred. No. 4.5e-117;
 Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQAISEAFADFLAGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 Db 1 MTEQAISEAFADFLAGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 QY 1 MTEQAISEAFADFLAGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 Db 1 MTEQAISEAFADFLAGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 QY 61 IPKEQGLSEFWRGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 Db 61 IPKEQGLSEFWRGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120

Db 61 IPKEQGLSEFWRGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGSKGERERGLDCLVKTTSKDSGRGLYOGFSVS 180
 Db 121 GAAGATSLCFYYPIDFARTRLAADVGSKGERERGLDCLVKTTSKDSGRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTIVSWMIAQTAVAGVSYPPDVTYRRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTIVSWMIAQTAVAGVSYPPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGVDWCWKIFRDEGKAFKFGAMSVNLKMGAFVLYLYDELKVI 298
 Db 241 QSGRKGADIMYTGVDWCWKIFRDEGKAFKFGAMSVNLKMGAFVLYLYDELKVI 298

RESULT 8

S31814
 ADP/ATP carrier protein T2 - mouse
 N:Alternate names: adenine nucleotide translocase
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change 09-Apr-1998
 C:Accession: S31814
 R:Costet, P.; Laplace, C.
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S31814
 A:Accession: S31814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <COS>
 A:Cross-references: EMBL:X70847
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;
 Best Local Similarity 89.2%; Pred. No. 1e-116;
 Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQAISEAFADFLAGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 Db 1 MTEQAISEAFADFLAGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 QY 61 IPKEQGLSEFWRGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 Db 61 IPKEQGLSEFWRGNLANVIRYFPQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGSKGERERGLDCLVKTTSKDSGRGLYOGFSVS 180
 Db 121 GAAGATSLCFYYPIDFARTRLAADVGSKGERERGLDCLVKTTSKDSGRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTIVSWMIAQTAVAGVSYPPDVTYRRMM 240
 Db 181 VGGIIIRAAVFGVYDPAKGLPDPKNTHTIVSWMIAQTAVAGVSYPPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGVDWCWKIFRDEGKAFKFGAMSVNLKMGAFVLYLYDELKVI 296
 Db 241 QSGRKGADIMYTGVDWCWKIFRDEGKAFKFGAMSVNLKMGAFVLYLYDELKVI 296

RESULT 9

S31935
 ADP/ATP carrier protein - African malaria mosquito
 C:Species: Anopheles gambiae (African malaria mosquito)
 C>Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
 C:Accession: S31935; S31936
 R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
 submitted to the EMBL Data Library, February 1993
 A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
 A:Reference number: S31935

A: Experimental source: clone T27E9
C: Geneties:
A: Gene: CESP:T27E9.1
A: Map position: 3
A: Introns: 20/1: 41/3: 115/2
C: Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

Query Match	67.3%	Score 1038;	DB 2;	Length 300;
Best Local Similarity	69.28;	Pred. No. 2.8e-84;		
Matches 202; Conservative	37;	Mismatches 49;	Indels 4;	Gaps 3

[illegible]

RESULT 13

T15206
 hypothetical protein W02D3.6 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
 C:Accession: T15206
 R:Id: T.; Weinstock, L.; Rifkin, L.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid W02D3.
 A:Reference number: Z18308
 A:Accession: T15206
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-300 <LE>
 A:Cross-references: EMBL:AF003141; NID:G2088732; PID:G2088738; PIDN:AA54179.1; GSPDB:GN
 A:Experimental source: strain Bristol N2; clone W02D3
 C:Genetics:
 A:Gene: CESP:W02D3.6
 A:Map position: 1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 <9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match	64.48;	Score 993.5;	DB 2;	Length 300;
Best Local Similarity	64.88;	Pred. No. 2.4e-80;		
Matches 195;	Conservative 40;	Mismatches 59;	Indels 7;	Gaps 4;

```

0Y      2  TEOAISFK---DEFLAGIAAISKTVAPIERKLLLOVHANSKOJAAOKYKGVDCI  58
      1  : : : : : | - | : : : : : | : : : : : | : : : : : | : : : : : |
Db      3  TKEGDYKRLPVLDAAGTAAISKTVAPIERKLLLOVSDVSEYVTAARKKKGIMDYL  62
      1  : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
0Y      59  VRIPEQGVLSFMKGNLANVRYEPPTOALNFAFKYKOJLEGLGVDKHOFMKRYFAGNLA  118
      1  : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db      63  ARVREKQGYAFMKGNLANVRYEPPTOALNFAFKYKJLEGLGVDKHOFMKRYFAGNLA  122
      1  : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
0Y      119  SGAAGATSLCFFVYPLDFARTRLADYKSGSTREPERFGLDCLVKTIRKSDIGILVQGS  178
      1  : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db      123  SGAAGATSLCFFVYPLDFVTRRLADYKGVDFEFGGLDCLFKYKISGPIGLVGRFP  181
      1  : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
0Y      179  VSVQIIYYRAAYGCVYDTAKGML-PDPKNTHIYVSMIAQVTAAGVSVYEPFDIVRRR  237
      1  : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

Dd	: : : : :
182	VSVGGIIYYRAAFGMFEPTAKTLSTDOQKINFTTVAIAOVGTVSGSYSPMDIVRRR
Qy	MMMSGRKGADIMYTGIVDCWRKIIFRDGGKAFFKGSAMNVLROMGSAFVLYVIDELKV
238	: : : : : :
Dd	MMMSGRR-DILKKNLTDCVRKLVKNGSLATLKKGLSNVFATGCALVLTVIDEIQHL
242	
Qy	296 I 298
Dd	300 I 300

RESULT 14

A161677
ADP, ATP carrier protein - Chlorella kessleri
C:Species: Chlorella kessleri
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C:Accession: A161677
R:Hitgarch, C.; Sauer, N.; Tanner, W.
J. Biol. Chem. 266, 24044-24047, 1991
A:Title: Glucose increases the expression of the ATP/ADP translocator and the glycerate
A:Reference number: A161677; MUID:92084708
A:Accession: A161677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <Hit>
A:Cross-references: GB:M6669; NID:9516596; PIDN:AAA31027.1; PID:9516597
C:Keyword: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
E:38-134/Domain: ADP, ATP carrier protein repeat homology <ACP1>
E:144-235/Domain: ADP, ATP carrier protein repeat homology <ACP2>
E:241-339/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match	63.48;	Score 978;	DB 2;	Length 339;
Best Local Similarity	66.98;	Pred. No. 6.4e-79;		
Matches 198; Conservative	26;	Mismatches 64;	Indels 8;	Gaps 5

[illegible]

RESULT 15

S51132
ADP/ATP carrier protein - malaria parasite (Plasmodium falciparum)
N:Alternate names: ADP/ATP transporter
C:Species: Plasmodium falciparum
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
C:Accession: S68993; S51132
R:Ratin, I.; Jaureguiberry, G.
Eur. J. Biochem. 228, 86-91, 1995
A:Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human malarial parasite Plasmodium falciparum
A:Reference number: S68993; MUID:55188918
A:Accession: S68993
A:Status: preliminary
A:Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: April 29, 2001, 11:35:20 ; Search time 18.75 seconds
(without alignments)
908.514 Million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MTEQAIISPAKDFLAGGIAA.....LRMGCAFLVLYDEIKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues
Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /SID56/gcgdata/geneseq/AA1980.DAT:*
 - 2: /SID56/gcgdata/geneseq/AA1981.DAT:*
 - 3: /SID56/gcgdata/geneseq/AA1982.DAT:*
 - 4: /SID56/gcgdata/geneseq/AA1983.DAT:*
 - 5: /SID56/gcgdata/geneseq/AA1984.DAT:*
 - 6: /SID56/gcgdata/geneseq/AA1985.DAT:*
 - 7: /SID56/gcgdata/geneseq/AA1986.DAT:*
 - 8: /SID56/gcgdata/geneseq/AA1987.DAT:*
 - 9: /SID56/gcgdata/geneseq/AA1988.DAT:*
 - 10: /SID56/gcgdata/geneseq/AA1989.DAT:*
 - 11: /SID56/gcgdata/geneseq/AA1990.DAT:*
 - 12: /SID56/gcgdata/geneseq/AA1991.DAT:*
 - 13: /SID56/gcgdata/geneseq/AA1992.DAT:*
 - 14: /SID56/gcgdata/geneseq/AA1993.DAT:*
 - 15: /SID56/gcgdata/geneseq/AA1994.DAT:*
 - 16: /SID56/gcgdata/geneseq/AA1995.DAT:*
 - 17: /SID56/gcgdata/geneseq/AA1996.DAT:*
 - 18: /SID56/gcgdata/geneseq/AA1997.DAT:*
 - 19: /SID56/gcgdata/geneseq/AA1998.DAT:*
 - 20: /SID56/gcgdata/geneseq/AA1999.DAT:*
 - 21: /SID56/gcgdata/geneseq/AA2000.DAT:*
 - 22: /SID56/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1 *	1543	100.0	298	21	Y71033 Human adenine nucl
2	1454	94.2	298	21	Y71032 Human adenine nucl
3	1412	91.5	298	19	W61169 Anti protein. Mus
4	1385.5	89.8	297	21	Y71031 Human adenine nucl
5	742.5	48.1	346	21	G36577 Arabidopsis thalia
6	742.5	48.1	346	21	G37261 Arabidopsis thalia
7	742.5	48.1	346	21	G37264 Arabidopsis thalia
8	742.5	48.1	346	21	G38460 Arabidopsis thalia
9	742.5	48.1	363	21	G36576 Arabidopsis thalia
10	742.5	48.1	363	21	G37260 Arabidopsis thalia
11	742.5	48.1	363	21	G37263 Arabidopsis thalia

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	Y71033	1543	100.0	298	21	Y71033 Human adenine nucleotide translocator ANF3.
2	Y71033	1454	94.2	298	21	Y71032 Human adenine nucleotide translocator ANF3.
3	Y71033	1412	91.5	298	19	W61169 Anti protein. Mus
4	Y71033	1385.5	89.8	297	21	Y71031 Human adenine nucleotide translocator ANF3.
5	Y71033	742.5	48.1	346	21	G36577 Arabidopsis thalia
6	Y71033	742.5	48.1	346	21	G37261 Arabidopsis thalia
7	Y71033	742.5	48.1	346	21	G37264 Arabidopsis thalia
8	Y71033	742.5	48.1	346	21	G38460 Arabidopsis thalia
9	Y71033	742.5	48.1	363	21	G36576 Arabidopsis thalia
10	Y71033	742.5	48.1	363	21	G37260 Arabidopsis thalia
11	Y71033	742.5	48.1	363	21	G37263 Arabidopsis thalia

XX	Andersen CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Sabo TR,
PI	Ghosh SS;
DR	WPI: 2000-365619/31.
DR	N-PSDB: D00521.
XX	
XX	Recombinant construct encoding adenine nucleotide translocator
PT	polypeptide, useful e.g. in screening for potential therapeutic agents
PT	against mitochondrial disease
XX	
PS	Claim 46; Page 173-174; 175pp: English.
XX	
CC	The patent discloses a method to produce adenine nucleotide translocator
CC	(ANT) proteins or ANT fusion proteins using recombinant expression
CC	constructs. ANT is a nuclear encoded protein and a major component of
CC	inner mitochondrial membrane. It mediates transport of adenosine
CC	di/tri-phosphates across the mitochondrial inner membrane and also serve
CC	as an important molecular component of the mitochondrial permeability
CC	transition pore, a modulator of apoptosis. ANT is used to identify agent(s)
CC	or ligands that bind to, or interact with it. The ANT ligands are used to
CC	detect or isolate ANT in a biological sample, and therapeutically for
CC	regulating mitochondrial pore activity, for treating diseases associated
CC	with altered mitochondrial function, including Alzheimer's, Parkinson's
CC	and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC	Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC	encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC	disorders, mitochondrial diabetes and deafness (MIND), and myoclonic
CC	epilepsy, red ragged fibre syndrome. The present sequence is an
CC	adenine nucleotide translocator ANT3 from human brain.
XX	
XX	Sequence 298 AA;
XX	

XX	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD.
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	
OS	Homo sapiens.
XX	
PN	WO200026370-A2.
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
XX	08-SEP-1999; 99US-0393441.
PA	(MITO-) MITOKOR.
PI	Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI	Ghosh SS;
XX	
DR	WPI; 2000-365619/31.
XX	
DR	N-PSDB; D00520.
XX	
PT	Recombinant construct encoding adenine nucleotide translocator
PT	polypeptide, useful e.g. in screening for potential therapeutic agents
XX	against mitochondrial disease
XX	
PS	Claim 45; Page 172-173; 175pp; English.
XX	

	Query March	100.0%	Score 154.3	DB 21	Length 298
	Best Local Similarity	100.0%	Pred. NO.1.8e-157		
	Matches 298	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 MTEQAISEAFKPEFLAGGIAIAISKTAVAPIERKKLLDLYQHASKQIAADKOYKGIIVDCIVR 60				
Db	1 mteqaisfakfflbggiaaaisktavapiervklllyqghaskqiaadkqykgivdcivr 60				
QY	61 IPEQGVLSFWRGNLANVIRYPTQALNFAEKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120				
Db	61 ipkegvlsfwrghlanviryfpqgnalfatkdkykgqflfvgvdkhtcfwyfagnlasg 120				
QY	121 GAAGATSLCFYVPLDFAFATRLAADVGKSGTEREEREGLCDCLVTKTSNGINGLQGESVS 180				
Db	121 gaagatslcfvypldfattrlaadvgksgeterefrlgdcivklksdgrlrglyvgfavs 180				
QY	181 VGGIITVAAAFEGVYDTRKGMLPDPRKNHIVYNNMIAQTVANAVGVSVSPEDTVRRMM 240				
Db	181 vggililyaaafgyvydtkagmlpdknhiavswmlaqtlavagvsyptdvtvrrmm 240				
QY	241 QSGRGADIMVTGWDCKRKIFRDEGSKAFKFGAMSNVLRMGAGFVLYLDELKVI 298				
Db	241 qsgrtgadimvtgvdckrklfrdegskafkfgamsnvlrmgagfvlvlydelkvi 298				
RESULT	2				
	Y71032				
ID	Y71032 standard; protein; 298 AA.				
XX	YC71032;				
DT	29-AUG-2000 (first entry)				
XX					
DE	Human adenine nucleotide translocator ANF2.				
XX					
KW	Human; adenine nucleotide translocator; ANF2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MP; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;				

[illegible]

Db	241	qsgrrgtclmtygtldcwrkrlardeggkaffkagwsvnlrgmgafvlylvgelrk	296
RESULT	3		
ID	W61169		
XX	W61169	standard; Protein; 298 AA.	
AC	W61169;		
DT	28-SEP-1998	(first entry)	
XX			
DE	Anti protein.		
XX			
KW	Anti; Adenine nucleotide translocator; cloning; screening;		
KW	DNA tag dideoxy terminator cycle sequencing; oxidative phosphorylation;		
KW	Prob; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;		
KW	hypertrrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;		
XX	lactic acidosis; degenerative muscle disease.		
XX			
OS	Mus sp.		
XX			
PN	MO9819714-A1.		
XX			
PD	14-MAY-1998.		
PF	31-OCT-1997; 97MO-US19882.		
XX			
PR	01-NOV-1996; 96US-0030017.		
PA	(UYEM-) UNIV EMORY.		
PI	Graham BC, Macgregor GR, Wallace DC;		
XX			
DR	WPI: 1998-286608/25.		
DR	N-PSDB: V36479.		
PT	Mice lacking heart-muscle adenine nucleotide translocator protein -		
PT	useful as model for mitochondrial myopathy and hypertrophic		
PT	cardiomyopathy in animals and to test therapeutic compositions or		
PT	gene therapies		
PS	Disclosure; Page 39-40; 61pp; English.		
XX			
CC	The present sequence is the mouse Anti protein, the cDNA producing this		
CC	polypeptide is cloned by screening a mouse heart cDNA library with the		
CC	human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA		
CC	tag dideoxy terminator cycle sequencing. The Anti protein is encoded by		
CC	the Anti locus, a nuclear gene on chromosome 8. This protein is required		
CC	in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP		
CC	which can then be converted into ATP. An Anti homozygous mutant would		
CC	thus be defective in OXPHOS which results in disease in oxidative		
CC	metabolism dependent tissues. This mouse Anti homozygous mutant can be		
CC	used as a model system for fascioscapular humeral muscular dystrophy,		
CC	hypertrrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model		
CC	systems can be used to test possible therapeutic compounds which		
CC	increase/mediate ATP and ADP exchange across the mitochondrial membrane		
CC	independent of ANTI.		
XX			
SO	Sequence 298 AA;		
Query: Match	91.5%;	Score 1412;	DB 19; Length 298;
Best Local Similarity	88.6%;	Pred. No. 2,1e-143;	
Matches 264;	Conservative 19;	Mismatches 15;	Indels 0; Gaps 0;
OY	1	MTEQASIFAKNOFLAGGIAAISTKTVAPRIERKLLLYOVHASKQIADAKQYGYDCIYR	60
DB	1	mgdgalstlktldlaggiaaavsktavprierklllyqvhaskqisaekyxgildcivr	60
OY	61	IPKEGVGSFPMNGNLANYIRYPTQALNPNAPFDXKQJFGLGVNDHPTQWRPFAGNLASG	120
DB	61	lpkeggflstfvrnglananyirypcgaiafaikdkyqgfligvvdthkqtwryfegnlasg	120

Oy	121	GAATATLCCVYPLDPRRLADVKSCHREERFRLGCLVIRKSDGIRLQVGFSSV	180
Db	121	gaagatcctcvtpldfrtllaaadvkqssqrefngldcltktkrsdglxglvygfvss	180
Oy	181	VQGIITRAAYFCGYDTAKGMLDPKNTHTIIVYSMMIAQTVAIVAGVSYPEDTVRRMM	240
Oy	241	QSGKKGADIMYTGIVDCMKRIFDEBGGKAFPGKGSNNVLRGGCAFVLVDELKKVI	298
Db	241	qsqrkgadimltyglldcwrklakdeganaflkfgawsnvlrimgafvlvlydelkkvv	298
RESULT	4		
ID	Y71031	standard; Protein: 297 AA.	
AC	Y71031:		
DE	29-AUG-2000	(first entry)	
XX		Human adenine nucleotide translocator ANTL1.	
XX		Human: adenine nucleotide translocator: ANTL1; mitochondria; ADP; ATP;	
KW		adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
KW		mitochondrial permeability transition; neuroprotective; nocrotic;	
KW		antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW		antipariatic; cerebroprotective; therapeutic; screening; psoriasis;	
KW		Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW		diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW		mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW		mitochondrial diabetes and deafness; hyperproliferative disorder;	
KW		myoclonic epilepsy red ragged fibre syndrome.	
XX			
OS		Homo sapiens.	
PN		MO200026370-A2.	
PD		11-MAY-2000.	
XX			
PF		03-NOV-1999; 99MO-US25883.	
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XX		03-NOV-1998; 98US-0185904.	
PR		08-SEP-1999; 99US-0393441.	
XX			
PA		(MITO-) MITOKOR.	
P1		Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;	
P1		Ghosh SS;	
DR		N-PSDB: D00519.	
XX			
XX		WPI: 2000-365619/31.	
PT		Recombinant construct encoding adenine nucleotide translocator	
PT		polypeptide, useful e.g. in screening for potential therapeutic agents	
PT		against mitochondrial disease	
XX			
PS		Claim 44: Page 172: 175pp: English.	
XX			
CC		The patent discloses a method to produce adenine nucleotide translocator	
CC		(ANT) proteins or ANT fusion proteins using recombinant expression	
CC		constructs. ANT is a nuclear encoded protein and a major component of	
CC		inner mitochondrial membrane. It mediates transport of adenosine	
CC		dlt/r1-phosphates across the mitochondrial inner membrane and also serves	
CC		as an important molecular component of the mitochondrial permeability	
CC		transition pore, a modulator of apoptosis. ANT is used to identify agents	
CC		or ligands that bind to, or interact with it. The ANT ligands are used to	
CC		detect or isolate ANT in a biological sample, and therapeutically for	
CC		regulating mitochondrial pore activity, for treating diseases associated	
CC		with altered mitochondrial function, including Alzheimer's, Parkinson's	
CC		and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,	
CC		Leber's hereditary optic neuropathy, schizophrenia, mitochondrial	

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AC G38460;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 47451.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
PD
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XX 06-SEP-2000.
PF
XX 25-FEB-2000; 2000EP-0301439.
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KM termination sequence.
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